AMENDMENTS TO THE CLAIMS:

This listing of the claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. *(currently amended)* A method for providing an integrated genetic and physical map of a genome or a part thereof, the method comprising the steps of:

(a) providing at least two individual genetic markers for the genome or a part thereof~~,~~ ~~preferably~~ in the form of a genetic map;

(b) ~~characterising the genetic markers by means of~~ identifying at least one AFLP fragment characterizing each genetic marker by means of ~~identified through~~ AFLP fingerprinting employing at least one forward AFLP primer and at least one reverse AFLP primer;

(c) providing a library of clones comprising fragments of the genome or a part thereof, ~~preferably~~ which is an artificial chromosome library ~~such as a BAC or YAC~~;

(d) generating a multitude of pools, each pool containing a multitude of individual clones from the library;

(e) generating an AFLP fingerprint for each of the pools employing forward AFLP primers and reverse AFLP primers;

(f) identifying in the multitude of pools a pool in which an AFLP fragment that was identified in step (b) is present in the fingerprint of the pool;

(g) generating an AFLP fingerprint for each of the individual clones in the pool identified in step (f) employing forward AFLP primers and reverse AFLP primers, and identifying the clone containing the AFLP fragment identified in step (b) in [[its]] such clone's AFLP fingerprint;

(h) generating a contig comprising the individual clone identified in step (g);

(i) repeating steps (f) - (h) for at least a second AFLP fragment identified in step (b) whereby the second, or a further, AFLP fragments ~~characterise~~ characterizes a second, or a further, genetic marker; and,

(j) linking at least two [[of the]] contigs obtained in step (h); [[to]] thereby obtaining said [[an]] integrated genetic and physical ~~and genetic~~ map of the genome or a part thereof, which comprises at least two genetic markers;

wherein

(1) the forward ~~and reverse~~ AFLP primers used in steps (b) and (e) comprise K ~~respectively L~~ selective nucleotides at the 3'-end ~~of the primers~~,

(2) the reverse AFLP primers used in steps (b) and (e) comprise L selective nucleotides at the 3'-end,

(3) ~~wherein~~ the forward ~~and reverse~~ AFLP primers used in step (g) comprise M ~~respectively N~~ selective nucleotides at the 3'-end ~~of the primers~~, and

(4) the reverse AFLP primers used in step (g) comprise N selective nucleotides at the 3' end, and

wherein K, L, M, N are integers with a value from 0 to 10, and ~~wherein K+L≥M+N~~ (K+L) > (M+N).

2. *(currently amended)* A method for linking a genetic marker to a physical marker in a genome or a part thereof, the method comprising the steps of:

(a) characterizing ~~characterising~~ the genetic marker by means of at least one AFLP fragment identified through AFLP fingerprinting employing at least one forward AFLP primer and at least one reverse AFLP primer;

(b) providing a library of clones comprising fragments of the genome or a part thereof~~, preferably~~ which is an artificial chromosome library ~~such as a BAC or YAC~~;

(c) generating a multitude of pools, each pool containing a multitude of individual clones from the library;

(d) generating an AFLP fingerprint for each of the pools employing forward AFLP primers and reverse AFLP primers;

(e) identifying in the multitude of pools a pool in which an AFLP fragment identified in step (a) is present in the fingerprint of the pool;

(f) generating an AFLP fingerprint for each of the individual clones in the pool identified in (e) employing forward AFLP primers and reverse AFLP primers, and identifying the clone containing the AFLP fragment identified in (a) in its AFLP fingerprint;

(g) generating a contig comprising the individual clone identified in step (f),

thereby linking the genetic marker to a physical marker;

wherein

(1) the forward ~~and reverse~~ AFLP primers used in steps (a) and (d) comprise K ~~respectively L~~ selective nucleotides at the 3'-end ~~of the primer~~,

(2) the reverse AFLP primers used in steps (a) and (d) comprise L selective nucleotides at the 3'-end,

(3) ~~wherein~~ the forward ~~and reverse~~ AFLP primers used in step (f) comprise M ~~respectively N~~ selective nucleotides at the 3'-end ~~of the primer~~, and

(4) the reverse AFLP primers used in step (f) comprise N selective nucleotides at the 3' end, and

wherein K, L, M, N are integers with a value from 0 to 10, and ~~wherein K+L≥M+N~~ (K+L) > (M+N).

3. *(currently amended)* The method according to claim 2, wherein steps (a)-(g) are repeated for additional ~~further~~ genetic markers in the genome or a part thereof and wherein the contigs obtained in (g) are aligned to ~~thereby~~ obtain an integrated physical and genetic map.

4. *(currently amended)* The method according to claim 1~~any one of claims 1-3~~, wherein the sum (K+L) minus the sum [[–]] (M+N) is at least 2~~, preferably at least 3, more preferably at least 4~~.

5. *(currently amended)* The method according to claim 4, wherein the sum M+N is at least 0~~, preferably at least 1, more preferably at least 2, most preferably at least 3~~.

6. *(currently amended)* The method according to claim 5~~claims 1-5~~, wherein each pool contains at most 0.6 genome equivalents of the total genome [[to be]] being analyzed ~~analysed, preferably 0.5 more preferably 0.4, most preferably 0.3~~.

7. *(currently amended)* The method according to claim 6~~claims 1-6~~, further comprising an additional pooling step.

8. *(currently amended)* The method according to claim 7 ~~claims 1-7~~, wherein the genetic markers are provided with a density of at least one genetic marker per 100 kb.

9. *(currently amended)* The method according to claim 8, wherein the contigs are aligned using a computer program suitable for such aligning ~~such as FPC~~.

10. *(currently amended)* The method according to claim 9, wherein the artificial chromosome library contains at least 5 genome equivalents.

11. to 14. (Canceled)

15. *(new)*. The method according to claim 1, wherein the artificial chromosome library is a BAC library or a YAC library.

16. *(new)*. The method according to claim 2, wherein the artificial chromosome library is a BAC library or a YAC library.

17. *(new)* The method according to claim 1, wherein the sum (K+L) minus the sum (M+N) is at least at least 3.

18. *(new)* The method according to claim 1, wherein the sum (K+L) minus the sum (M+N) is at least at least 4.

19. *(new)* The method according to claim 4, wherein the sum M+N is at least 1

20. *(new)* The method according to claim 4, wherein the sum M+N is at least 2

21. *(new)* The method according to claim 4, wherein the sum M+N is at least 3

22. *(new)* The method according to claim 5, wherein each pool contains at most 0.5 genome equivalents of the total genome being analyzed.

23. *(new)* The method according to claim 5, wherein each pool contains at most 0.3 genome equivalents of the total genome being analyzed.

24. *(new)* The method according to claim 8 wherein the computer program is FPC.